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Scientific Article

Combining ability of soybean in F_1 and F_2 generations for earliness and grain yield

Capacidade combinatória de soja em F_1 e F_2 visando precocidade e produção de grãos

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ABSTRACT – Parental selection is a key step in genetic improvement programs, as it impacts the genetic potential of the segregating population and the genetic progress that can be achieved. This selection can be made through predictive or diallel analyses, which estimate general (GCA) and specific combining abilities (SCA). This study evaluated F_1 and F_2 soybean (Glycine max) populations derived from diallel crosses to select parents for traits related to earliness, production components, and grain yield. Fifteen treatments were analyzed in a randomized complete block design, including 10 biparental combinations and 5 parent lines (TMG 801, TMG 803, BRS 511, UFUS 7101, and UFUS 7201). Traits assessed were days to flowering and maturity, plant height at maturity, height of first-pod insertion, number of nodes at maturity, branched nodes, productive nodes, pods with one, two, and three grains, total pods per plant, seeds per pod, and grain yield. Results indicated that evaluating the F_1 generation was sufficient, as parent characteristics were consistent in the F_2 generation. The diallel analysis identified promising combinations for reducing the growth cycle and increasing productivity and grain yield. BRS 511 x TMG 803, UFUS 7201 x TMG 803, and TMG 803 x UFUS 7101 showed the greatest potential.

Keywords: Diallel crosses. Genetic improvement. Parental selection.

RESUMO – A seleção de genitores é uma das etapas fundamentais de um programa de melhoramento genético, pois influencia o potencial genético da população segregante gerada, refletindo consequentemente nos progressos genéticos a serem alcançados. Estes, por sua vez, podem ser selecionados por análises preditivas e/ou análises dialélicas, que permitem estimar as capacidades gerais (CGC) e específicas (CEC) de combinação. Nesta pesquisa, objetivou-se avaliar populações F_1 e F_2 de soja (*Glycine max*) provenientes de cruzamentos dialélicos para a seleção de genitores visando à precocidade, componentes de produção e produção de grãos. Em delineamento de blocos ao acaso, analisaram-se 15 tratamentos, sendo 10 combinações biparentais e 5 genitores (TMG 801, TMG 803, BRS 511, UFUS 7101 e UFUS 7201). Os caracteres avaliados foram número de dias para o florescimento e maturidade, altura da planta na maturidade, altura de inserção da primeira vagem, número de nós na maturidade, número de nós ramificados, número de nós produtivos, número de vagens com um, dois e três grãos, número de vagens por planta, número de sementes por vagem e produção de grãos. A avaliação da geração F_1 é suficiente visto que, a consistência nas características dos genitores se manteve na F_2. Com a análise dialélica foi possível identificar as combinações mais promissoras para reduzir o ciclo e aumentar a produtividade e a produção de grãos. Destacam-se as combinações BRS 511 x TMG 803, UFUS 7201 x TMG 803 e TMG 803 x UFUS 7101 como as mais promissoras sucessivamente.

Palavras-chave: Cruzamentos dialélicos. Melhoramento genético. Seleção de genitores.

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INTRODUCTION

The productive success of soybeans [*Glycine max* (L.) Merr.] in Brazil is largely driven by genetic improvement programs that develop cultivars that meet producer demands. Soybean has achieved high productivity across regions due to the development of cultivars with greater yields and resistance to biotic and abiotic stress factors (SILVA et al., 2020). In the 2022/23 growing season, Brazil established itself as a global leader in soybean production, reaching a volume of 152.71 million tons of grain (CONAB, 2023).

The diallel cross is a widely used strategy for selecting parents in the improvement of self-pollinating species like soybean, as proposed by Griffing (1956). These crosses provide genetic insights into traits, aiding in the management and selection of segregating populations (GERHARDT et al., 2019) and facilitating the estimation of general (GCA) and specific combining abilities (SCA).

GCA and SCA estimates reveal the gene action involved in trait inheritance, guiding the selection of superior progeny in initial generations or if needed, the advancement to later generations. Predominantly high GCA values are desirable, as they relate to additive gene effects the heritable fraction of the genotype. In contrast, SCA reflects gene interactions related to non-additive effects among parents (CRUZ; REGAZZI; CARNEIRO, 2012; THUNGO; SHIMELIS; MASHILO, 2022). These estimates enable breeders to identify the best parental combinations with a high probability of generating promising segregating populations for superior line development (RAMALHO et al., 2012).

Diallel analyses generally focus on F_1 hybrids; however, early soybean generations face a limitation in F_1 seed quantity due to the challenges of artificial hybridization (DARONCH et al., 2014). Therefore, studies incorporating diallel analysis in both F_1 and F_2 generations provide critical data for assessing soybean parents in breeding programs, allowing breeders to evaluate the relevance and consistency of obtained estimates, thus informing their decisions.

This study aimed to evaluate F_1 and F_2 soybean populations derived from diallel crosses to select parents for traits related to earliness, production components, and grain yield.

MATERIAL AND METHODS

The experiment was conducted from 2021 to 2023 in a greenhouse at Fazenda Experimental Capim Branco (18°57′ 30″ S, 48°12′0″ W), part of the Federal University of Uberlândia (UFU), located in the southwestern region of Minas Gerais, Brazil. Five soybean cultivars (TMG 801, TMG 803, BRS 511, UFUS 7101, and UFUS 7201) were evaluated as potential parents for the Research Center for Soybean Genetics and Breeding (Melhor Soja –UFU), focusing on the development of conventional cultivars with resistance to Phakopsora pachyrhizi (Asian soybean rust–ASR). Three of these parents (TMG 801, TMG 803, and BRS 511) exhibit partial genetic resistance to ASR, with results supported by previous research (GODOY, 2009; MELO et al., 2017). The lines UFUS 7101 and UFUS 7201 have shown promising performance in *Melhor Soja*–UFU trials.

The crossing block was conducted in a greenhouse from September 2021 to July 2022. Sowing was done in 3.0-dm^3 polyethylene pots filled with a mixture of commercial substrate, soil, and cattle manure (3:1:1). The soil had the following chemical properties: pH (H_2O): 5.7; P Meh: 5.5 mg dm^{-3}; K^+: 243.9 mg dm^{-3}; Ca^{2+}: 0.62 cmolc dm^{-3}; Mg^{2+}: 1.53 cmolc dm^{-3}; H+Al: 2.32 cmolc dm^{-3}; V: 65%. Particle distribution was as follows: sand 270 g kg^{-1}, silt 170 g kg^{-1}, and clay 560 g kg^{-1}.

To synchronize flowering among parents, sowing was staggered every three days, with a depth of 3.0 cm and five seeds per pot. Fertilization was applied 15 days after emergence at a rate of 300 mg phosphorus, 150 mg potassium, and 50 mg nitrogen per kg of substrate. Fertilizers were dissolved in water, with 10 mL applied to each pot. Thinning was performed at the V1 stage (FEHR; CAVINESS, 1977), leaving three plants per pot.

Artificial hybridization was conducted using a diallel scheme to create hybrid combinations (BORÉM et al., 2021). Sepals were removed from the female parent's flower buds to expose the stigma for manual pollination. The flower buds were labeled with maternal and paternal parent identities and the date of crossing.

During the 2022/23 growing season, an experiment was conducted with both hybrid combinations and parent lines. Treatments included 15 treatments: 10 F_1 hybrid combinations and 5 parents, arranged in a randomized complete block design with five replications. Each plot contained a 3-dm^3 pot with one plant under conditions similar to the crossing block. Sowing was done manually on September 22, 2022. Pots were irrigated daily and as needed to prevent waterlogging. Weeds and sludge buildup were managed regularly, and preventive measures were taken against pests and diseases. Bamboo stakes (1.5 m high) were used to support plant growth effectively.

Dates of emergence (VE), flowering (R1), and maturity (R8) were recorded based on the Fehr and Caviness (1977) scale. The following agronomic traits were measured for each plant: 1) Days to flowering (NDF) and maturity (NDM): calculated from VE to R1 and VE to R8, respectively; 2) Plant height at maturity (PHM): measured from the hypocotyl base to the last node on the main stem; 3) First pod insertion height (FPIH): measured from the hypocotyl base to the insertion node of the first pod; 4) Number of nodes at maturity (NNM): total node count on the main stem from the cotyledon node; 5) Number of branched nodes (NBN): count of all main stem nodes with branching; 6) Number of productive nodes (NPN): count of main stem nodes producing pods; 7) Number of pods with one (NP1G), two (NP2G), and three grains (NP3G): counted after manual harvest; 8) Total number of pods per plant (NPP): sum of NP1G, NP2G, and NP3G; 9) Number of seeds per pod (NSP): ratio of total seeds per plant to total pods per plant; and 10) Grain yield (GY): measured as grain mass per plot, using a digital scale with 0.01-g precision.

F_2 seeds from all combinations and parents were used to conduct a diallel evaluation in the F_2 generation. The second experiment, with the same F_1 treatments, included 19 blocks with two plants per plot, following Bagateli et al. (2020), who evaluated 30 F_2 plants in diallel studies in soybean. Sowing for the F_2 population was done on March 29, 2023, using the same procedures as the F_1 experiment, with two plants per pot, replicated in 19 blocks. The same traits were measured as in the F_1 generation.

Both experiments followed standard cultural practices and phytosanitary management as per technical recommendations for soybeans (EMBRAPA, 2014) under greenhouse conditions.

Data for each trait were analyzed individually for each generation (F_1 and F_2) through analysis of variance to determine genetic variability among populations. Mean estimates for each population and its parents and residual mean squares for diallel analysis were obtained. The statistical software GENES was used for the analysis (CRUZ, 2016).

Diallel analysis was performed using Griffing's (1956) method II, which includes hybrid and parental combinations, following the model $Y i j = \mu + G i + G j + S i j + \overline{\varepsilon_{ij}}$, where $Y i j$ is the mean value for the hybrid (i≠j) or parental combination (i=j) for each agronomic trait, μ is the overall mean effect, $G i$ and $G j$ are the general combining abilities of the $i^{\text{-th}}$ and $j^{\text{-th}}$ parents, respectively, $S i j$ is the specific combining ability for the cross between parents i and j, and $\overline{\varepsilon_{ij}}$ is the mean experimental error.

RESULTS AND DISCUSSION

The variance analysis revealed a significant effect at the 5% level by the F-test for all agronomic traits, confirming the presence of genetic variability among populations and parents in both the F_1 and F_2 generations (Table 1). This finding highlights the divergence among parents, which is crucial for hybridizations aimed at generating segregating populations beneficial for selection processes in breeding programs (RAMALHO et al., 2012).

The coefficients of variation (CV) ranged from 5.57% (NDM) to 41.67% (NBN) in the F_1 population and from 10.02% (NDM) to 46.22% (NBN) in the F_2 population. Low CV values indicate high experimental precision, with values up to 20% generally considered acceptable. This threshold is established by the Ministry of Agriculture, Livestock, and Food Supply for experiments related to soybean cultivar registration in Brazil. Only the traits PHM, FPIH, and NBN in the F_1 generation and PHM, FPIH, and NNR in the F_2 generation exceeded this accepted CV threshold (Table 1). It is worth noting that this study was conducted on early generations, and these populations will undergo selection for the targeted traits, leading to increased homogeneity and development of pure lines.

Table 1. Summary of variance analysis for agronomic traits, general combining ability (GCA), specific combining ability (SCA), and coefficient of variation (CV) in diallel analysis involving five soybean parents and their crosses in the F_1 and F_2 generations.

Source of variation	DF	Mean square						
		F_1						
		NDF	NDM	PHM	FPIH	NNM	NBN	NPN
Blocks	5	24.45	76.57	3848.03	38.52	16.15	25.33	16.23
Genotypes	14	169.48*	197.95*	2685.06*	108.61*	19.99*	12.97*	19.73*
Residual	70	19.51	52.60	494.80	24.32	4.92	4.16	6.14
Mean		41.83	130.19	102.34	19.20	14.82	4.9	12.91
CV (%)		10.56	5.57	21.73	25.68	14.97	41.67	19.19
GCA	4	378.12*	449.05*	5884.86*	207.10*	31.93*	32.12*	26.15*
SCA	10	86.03*	97.50^{ns}	1405.35*	69.26*	15.21*	5.33^{ns}	17.17*
		F_2						
Blocks	19	44.57	310.81	830.19	27.40	4.12	1.43	4.73
Genotypes	14	654.96*	1676.15*	8189.61*	342.51*	26.70*	22.07*	21.87*
Residual	266	46.19	127.99	608.29	28.06	3.43	1.46	2.97
Mean		35.38	112.91	92.69	15.28	11.56	2.62	9.33
CV (%)		19.21	10.02	26.61	34.68	16.03	46.22	18.47
GCA	4	2141.36*	5676.50*	21909.08*	1021.91*	68.14*	62.80*	56.89*
SCA	10	60.61^{ns}	76.13^{ns}	2701.38*	70.76*	10.12*	5.79*	7.86*

*Significant at a 5% probability by the F-test. ^{ns}: Non-significant. DF: Degrees of freedom; NDF: number of days to flowering; NDM: number of days to maturity; PHM: plant height at maturity; FPIH: first-pod insertion height; NNM: number of nodes at maturity; NBN: number of branched nodes; NPN: number of productive nodes.

The analysis of variance for production components and grain yield showed genetic variability at a 5% significance level by the F-test, indicating genetic differences among parents and their populations (Table 2). This suggests favorable conditions for soybean genetic improvement, enabling the selection of superior individuals from the F_2 generation.

The experimental coefficients of variation (CV) for production components and grain yield ranged from 8.80% (NSP) to 72.27% (NP1G) in the F_1 generation and from 10.04% (NSP) to 60.03% (NP1G) in the F_2 generation (Table 2). CV values were notably higher for traits related to pod count and grain yield, likely due to their polygenic inheritance and high environmental sensitivity. This aligns with findings by Gastl Filho et al. (2022), who studied segregating soybean populations and observed genetic variability for production components, with CVs exceeding 20%, reflecting the complexity of these traits.

The experimental coefficients of variation (CV) for production components and grain yield ranged from 8.80% (NSP) to 72.27% (NP1G) in the F_1 generation and from 10.04% (NSP) to 60.03% (NP1G) in the F_2 generation (Table 2). Higher CV values were observed for pod-related traits and grain yield, likely due to their polygenic nature and environmental sensitivity, supporting findings by Gastl Filho et al. (2022), who reported CVs above 20% for production components in segregating soybean populations.

Diallel crosses allow for estimates of GCA and SCA. GCA is primarily associated with additive gene effects, reflecting a parent's ability to combine well with various other parents (CRUZ; REGAZZI; CARNEIRO, 2012). SCA, conversely, relates to non-additive gene effects, emphasizing the unique interaction potential between two parents. This approach underlines the role of both additive and non-additive genetic effects in determining trait expression in cross-derived plants (CHAGAS et al., 2023).

Table 2. Summary of variance analysis for production components, grain yield, general combining ability (GCA), specific combining ability (SCA), and coefficient of variation (CV) in diallel analysis involving five soybean parents and their crosses in the F_1 and F_2 generations.

Source of variation	DF	Mean square					
		F_1					
		NP1G	NP2G	NP3G	NPP	NSP	GY
Blocks	5	18.92	253.14	504.38	1072.25	0.11	492.99
Genotypes	14	59.08*	3101.24*	650.46*	3614.90*	0.16*	484.61*
Residual	70	33.33	452.54	222.64	1126.86	0.03	181.93
Mean		7.99	39.97	25.01	73.18	2.24	28.33
CV (%)		72.27	53.23	59.66	45.87	8.80	47.61
GCA	4	93.66*	8604.84*	1043.02*	6299.09*	0.33*	687.29*
SCA	10	45.23^{ns}	899.56*	493.46*	2541.55*	0.09*	403.62*
		F_2					
Blocks	19	4.33	27.34	19.16	93.32	0.04	11.39
Genotypes	14	65.25*	529.81*	237.28*	812.91*	0.78*	108.45*
Residual	266	6.88	43.78	16.00	105.43	0.04	13.51
Mean		4.37	13.36	8.59	27.66	2.09	10.24
CV (%)		60.03	49.53	46.59	37.13	10.04	35.90
GCA	4	90.22*	1430.86*	673.57*	1904.47*	1.70*	322.72*
SCA	10	55.27*	169.40*	62.76*	376.29*	0.41*	22.74^{ns}

*Significant at a 5% probability level by the F-test. ^{ns}: Non-significant; DF: Degrees of freedom; NP1G: number of pods with one grain; NP2G: number of pods with two grains; NP3G: number of pods with three grains; NPP: total number of pods per plant; NSP: number of seeds per pod; GY: grain yield.

Traits related to growth cycle, height, and node count (Table 1) showed significant GCA effects at a 5% level (F-test) in both the F_1 and F_2 generations. SCA was significant for most traits, except for NDM and NBN (total cycle and number of branched nodes) in F_1 and for NDF and NDM (vegetative and total cycle) in F_2. For production components and grain yield, SCA was not significant for NP1G in F_1, and GY in F_2 also showed no statistical significance (Table 2).

The interpretation of significant GCA estimates depends on their magnitude and direction. The ideal parents for breeding purposes are those with high positive or negative GCA values, depending on whether the trait should be increased or decreased (CRUZ; REGAZZI; CARNEIRO, 2012; RAMALHO et al., 2012). High positive GCA values are desirable when aiming to increase a trait, while high negative values are preferred for traits targeted for reduction (e.g., NDM, NDF, and NP1G).

Table 3 presents the GCA effect estimates for each genotype. The parents BRS 511, UFUS 7201, and UFUS 7101 were notable for their GCA in the vegetative cycle in both F_1 and F_2 generations. Meanwhile, cultivars TMG 803 and TMG 801 showed higher GCA estimates for grain yield.

Selecting segregating populations through diallel trials involves analyzing GCA and SCA estimates (Table 3). In this sense, we aimed to select populations from parents with high GCA and SCA values (RAMALHO et al., 2012). Bezerra et al. (2017) reported similar results in diallel studies with soybeans, highlighting the presence of additive and dominance gene effects in traits related to the vegetative cycle, total cycle, and grain yield.

The GCA mean squares for the F_1 and F_2 populations were higher than those of SCA across all evaluated traits (Tables 1 and 2), suggesting that additive genetic variance was the dominant component, with additive effects playing the primary role in controlling these traits (DARONCH et al., 2014; THUNGO; SHIMELIS; MASHILO, 2022). While SCA represents a non-additive effect, impacting hybrid performance beyond the additive effects of the parents' GCA (MIRANDA FILHO, 2018), it also reflects genetic divergence among parents.

Comparing the F_1 and F_2 results revealed that GCA effects were predominant, exceeding SCA effects. The F_1 generation showed a significant influence of GCA, with even higher GCA estimates observed in the F_2 generation, which supports a favorable scenario for selection. Rocha, Pereira, and Vello (2018) similarly concluded that additive gene effects outweighed non-additive effects, with GCA mean squares consistently higher than SCA for all traits.

In research on genetic control of agronomic traits involving the cultivar TMG 801, Bezerra et al. (2023) observed additive and dominant effects for the vegetative and total cycles. The study further noted that the most promising populations had genotypic values above the experiment average, reinforcing TMG 801's suitability for grain yield.

TMG 803 (ASR-resistant) was a standout for traits like FPIH, NBN, and NP2G across F_1 and F_2 populations. Meanwhile, UFUS 7101 (an early cycle, high-yielding cultivar) excelled in NNM, NP1G, and NPN in both generations.

Table 3. Estimates of general combining ability (GCA) effects for agronomic traits, production components, and grain yield in F_1 and F_2 generations for five soybean parents grown in a greenhouse.

Trait	Generation	Parent					
		BRS 511	UFUS 7201	TMG 803	TMG 801	UFUS 7101	GCA
NDF	F_1	−4.14	−0.28	3.19	2.60	−1.36	8.54
	F_2	−3.09	−2.06	5.71	2.41	2.98	14.97
NDM	F_1	−3.88	−1.54	4.50	1.98	−1.07	9.44
	F_2	−5.19	−5.06	7.32	6.55	−3.61	39.63
PHM	F_1	−16.70	2.93	5.94	−6.26	14.09	128.33
	F_2	−12.21	−3.56	23.95	0.55	−8.73	152.14
FPIH	F_1	−1.05	−1.07	3.68	−1.94	0.39	4.35
	F_2	−1.40	−1.55	4.72	−0.18	−1.59	7.10
NNM	F_1	−0.42	−0.46	−0.37	−0.30	1.55	0.64
	F_2	−0.71	−0.77	0.42	0.30	0.76	0.46
NBN	F_1	−0.75	−0.58	0.97	0.94	−0.58	0.67
	F_2	−0.71	−0.10	0.76	0.61	−0.58	0.44
NPN	F_1	−0.33	−0.52	−0.42	−0.11	1.39	0.48
	F_2	−0.40	−0.89	0.18	0.45	0.66	0.39
NP1G	F_1	0.56	−0.92	2.32	−0.49	−1.47	1.44
	F_2	0.58	−0.75	1.05	−0.11	−0.76	0.60
NP2G	F_1	−8.45	−7.45	25.00	−0.95	−8.16	194.10
	F_2	−2.01	−2.43	5.17	1.05	−1.78	9.91
NP3G	F_1	−3.70	3.94	−6.91	3.18	3.49	19.53
	F_2	−1.76	0.31	−2.63	2.69	1.38	4.70
NPP	F_1	−11.47	−4.14	20.24	1.60	−6.23	123.15
	F_2	−3.32	−3.13	3.35	4.51	−1.40	12.85
NSP	F_1	−0.06	0.04	−0.12	0.05	0.09	0.01
	F_2	−0.08	0.10	−0.14	0.01	0.11	0.01
GY	F_1	−5.25	−1.37	5.61	1.92	−0.91	12.03
	F_2	−1.66	−1.19	1.40	1.73	−0.28	2.21

NDF: number of days to flowering; NDM: number of days to maturity; PHM: plant height at maturity; FPIH: first-pod insertion height; NNM: number of nodes at maturity; NBN: number of branched nodes; NPN: number of productive nodes; NP1G: number of pods with one grain; NP2G: number of pods with two grains; NP3G: number of pods with three grains; NPP: total number of pods per plant; NSP: number of seeds per pod; GY: grain yield.

In the F_1 population, UFUS 7101 was favorable for PHM, UFUS 7201 for NP3G, TMG 801 for NSP, and TMG 803 for NPP and GY. In the F_2 population, TMG 803 was favorable for PHM, and TMG 801 was prominent for NP3G, NPP, NSP, and GY.

Genetic improvement aims to develop high-yield, regionally adapted cultivars that mature earlier (BORÉM; MIRANDA; FRITSCHE-NETO, 2021; CARNEIRO; PEREIRA; ZAMBIAZZI, 2019; SILVA et al., 2018). The GCA analysis of NDF and NDM (Table 3) indicates that TMG 803 is associated with extended cycle duration in both generations. However, targeting the parent that contributes most to cycle reduction is recommended for the specific traits of interest, as early maturity can be advantageous.

In this study, the cultivar BRS 511 was identified as the parent most favorable for cycle reduction, as it exhibited a higher and more negative GCA estimate (Table 3). Silva et al. (2022) highlighted that early flowering and maturation are ideal for selecting genotypes, which aligns with the results here. Similarly, for reducing NP1G, UFUS 7101 emerged as the parent most effective at decreasing single-grain pod production.

Bezerra et al. (2017) studied TMG 801 and noted its tendency toward a longer cycle, making it a later-maturing cultivar. This observation is consistent with our findings in Table 3, where TMG 801 showed a delay in the cycle, second only to TMG 803. Both cultivars contributed to extended cycles in the F_1 and F_2 generations.

GCA and SCA estimates are now commonly used in soybean breeding to assess combining ability and gene expression. For example, Abebe et al. (2023) applied this analysis to biomass production, Pereira et al. (2018) used it for studying resistance to Asian soybean rust, and Colombo et al. (2018) focused on adaptation to Cerrado conditions. The goal remains to identify lines that are early-maturing, resistant, and high-yielding.

SCA reflects the performance of hybrids based on the GCA of their parents, relating to non-additive genetic effects (CRUZ; REGAZZI; CARNEIRO, 2012). Table 4 presents SCA effect estimates for various agronomic traits, while Table 5 provides estimates for production components and grain yield.

Table 4. Estimates of specific combining ability (SCA) effects for agronomic traits in five soybean parents grown in a greenhouse.

Combination		NDF	NDM	PHM	FPIH	NNM	NBN	NPN
BRS 511	F_1	2.29	−3.60	−7.55	0.99	−2.15	0.09	−1.92
-	F_2	−0.13	−1.67	−1.73	−1.97	−0.76	−0.13	−0.49
BRS 511 x UFUS 7201	F_1	2.93	7.56	11.92	−1.40	1.56	0.10	1.94
	F_2	2.45	3.40	10.93	3.68	1.8	0.06	1.34
BRS 511 x TMG 803	F_1	−4.38	−4.15	−6.30	−0.40	−0.53	−1.12	−0.83
	F_2	−3.51	0.64	−12.61	−0.34	−0.33	−0.73	−0.50
BRS 511 x TMG 801	F_1	−1.95	2.71	8.65	0.77	1.40	−0.43	1.36
	F_2	0.17	−2.14	1.98	−0.53	0.49	0.66	0.62
BRS 511 x UFUS 7101	F_1	−1.16	1.08	0.84	−0.95	1.87	1.26	1.36
	F_2	1.14	1.44	3.14	1.13	−0.43	0.26	−0.49
UFUS 7201	F_1	1.91	−0.27	−7.57	3.95	−0.39	−0.74	−1.04
-	F_2	−0.53	−0.85	−3.27	−1.12	−0.53	0.15	−0.55
UFUS 7201 x TMG 803	F_1	−6.74	−0.32	−13.43	−3.41	−2.15	−0.46	−1.97
	F_2	−1.26	−1.66	−3.36	−1.86	−0.26	0.39	0.18
UFUS 7201 x TMG 801	F_1	−0.47	−1.96	−15.24	−3.40	−0.39	0.91	−0.11
	F_2	−0.83	1.90	−1.60	0.21	−0.15	−0.41	−0.24
UFUS 7201 x UFUS 7101	F_1	0.48	−4.75	31.88	0.31	1.76	0.93	2.22
	F_2	0.71	−1.93	0.55	0.21	−0.32	0.25	−0.17
TMG 803	F_1	5.12	4.63	12.28	1.92	0.92	0.34	0.77
-	F_2	2.57	−0.25	8.57	2.39	0.13	−0.46	−0.26
TMG 803 x TMG 801	F_1	2.05	−2.67	8.11	4.98	0.52	1.36	0.30
	F_2	0.12	−0.52	0.92	1.25	−0.28	−0.14	−0.38
TMG 803 x UFUS 7101	F_1	−1.17	−2.13	−12.94	−5.02	0.32	−0.46	0.96
	F_2	−0.53	−0.49	2.35	−0.67	0.24	0.67	0.51
TMG 801	F_1	1.98	0.18	−2.58	−0.21	−0.39	−0.79	−0.68
-	F_2	0.12	−0.52	0.92	1.25	−0.28	−0.14	−0.38
TMG 801 x UFUS 7101	F_1	−3.57	1.57	3.65	−1.92	−0.75	−0.26	−0.18
	F_2	0.24	−0.72	1.30	−0.28	0.13	−0.55	0.06
UFUS 7101	F_1	2.71	2.11	−11.71	3.79	−1.60	−0.74	−2.18
-	F_2	−0.78	0.85	−3.68	−0.19	0.20	−0.32	0.05
SCA	F_1	−1.92	7.49	151.76	7.49	1.72	0.19	1.84
	F_2	−0.49	−2.59	104.66	2.13	0.33	0.22	0.24

NDF: number of days to flowering; NDM: number of days to maturity; PHM: plant height at maturity; FPIH: first-pod insertion height; NNM: number of nodes at maturity; NBN: number of branched nodes; NPN: number of productive nodes.

Table 5. Estimation of specific combining ability (SCA) effects for production components and grain yield in five soybean parents grown in a greenhouse.

Combination		NP1G	NP2G	NP3G	NPP	NSP	GY
BRS 511	F_1	1.73	0.93	−12.11	−9.92	−0.22	−6.53
-	F_2	2.20	0.41	−2.95	−0.96	−0.26	−0.769
BRS 511 X UFUS 7201	F_1	0.88	16.43	13.08	31.59	0.17	12.72
	F_2	−1.75	0.13	2.28	0.90	0.22	1.14
BRS 511 X TMG 803	F_1	−6.53	−26.69	1.27	−32.13	0.17	−9.36
	F_2	−2.11	−1.69	1.07	−2.98	0.15	−0.54
BRS 511 X TMG 801	F_1	0.45	−0.07	−1.99	−1.65	0.01	−1.05
	F_2	0.22	2.48	2.10	6.18	0.05	1.16
BRS 511 X UFUS 7101	F_1	1.75	8.47	11.87	22.02	0.08	10.75
	F_2	−0.76	−1.73	0.44	−2.18	0.10	−0.23
UFUS 7201	F_1	−2.32	−10.24	−10.40	−23.24	−0.07	−9.21
-	F_2	−0.73	−0.50	−0.88	−2.55	0.03	−0.59
UFUS 7201 X TMG 803	F_1	0.78	−4.69	−4.37	−8.46	−0.07	0.59
	F_2	2.36	2.00	0.48	4.73	−0.13	1.48
UFUS 7201 X TMG 801	F_1	2.75	2.43	1.37	6.35	−0.03	−0.88
	F_2	1.24	−0.70	−0.84	−0.34	−0.12	−1.18
UFUS 7201 X UFUS 7101	F_1	0.23	6.31	10.73	17.01	0.08	5.99
	F_2	−0.39	−0.42	−0.15	−0.19	−0.04	−0.26
TMG 803	F_1	1.70	12.36	3.32	17.50	0.04	3.91
-	F_2	−1.07	−4.49	−0.03	−5.37	0.04	−1.37
TMG 803 X TMG 801	F_1	1.68	7.48	−1.28	7.97	−0.07	3.19
	F_2	0.83	3.07	−2.32	1.11	−0.05	0.66
TMG 803 X UFUS 7101	F_1	0.66	−0.81	−2.26	−2.37	−0.11	−2.24
	F_2	1.07	5.60	0.84	7.88	−0.04	1.15
TMG 801	F_1	−1.51	−4.40	1.46	−4.39	0.05	−2.71
-	F_2	−1.64	−2.06	1.27	−2.61	0.09	−0.22
TMG 801 X UFUS 7101	F_1	−1.86	−1.03	−1.01	−3.89	0.00	4.16
	F_2	0.98	−0.73	−1.48	−1.73	−0.07	−0.20
UFUS 7101	F_1	−0.39	−6.47	−9.66	−16.39	−0.02	−9.33
-	F_2	−0.45	−1.36	0.18	−1.89	0.02	−0.23
SCA	F_1	1.98	74.50	45.14	235.78	0.01	36.95
	F_2	2.42	6.28	2.34	13.54	0.02	0.46

NP1G: number of pods with one grain; NP2G: number of pods with two grains; NP3G: number of pods with three grains; NPP: total number of pods per plant; NSP: number of seeds per pod; GY: grain yield.

Soybean breeding efforts aim to select early-maturing cultivars with high grain yield (BORÉM et al., 2021). The ideal approach in breeding is to choose parents with high pod production, a greater number of seeds per pod, and higher grain weight. As noted by Cruz, Regazzi, and Carneiro (2012), an optimal parent should bring both high GCA for selection and the desired SCA, ensuring the best hybrid combinations are achieved.

In this context, the crosses BRS 511 x TMG 803, UFUS 7201 x TMG 803, and TMG 803 x UFUS 7101 emerge as the most promising for optimizing both the growth cycle and productivity. These combinations are well-positioned to merge desirable GCA and SCA traits, supporting the goals of soybean breeding programs focused on high-yield and early-maturing cultivars.

CONCLUSION

Analyzing F_1 generation is enough to draw conclusions, as consistency in parent traits observed in F_1 is maintained in F_2. Diallel analysis effectively identifies the most promising combinations for cycle reduction and increases in production components and grain yield, with the combinations BRS 511 x TMG 803, UFUS 7201 x TMG 803, and TMG 803 x UFUS 7101 standing out. Genotype selection can be efficiently conducted in early generations for these populations, as additive gene effects predominate, making them highly promising for line extraction.

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